

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANTS: Alnemri, Emad S.  
Fernandes-Alnemri, Teresa  
Litwack, Gerald  
Armstrong, Robert  
Tomaselli, Kevin
- (ii) TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,  
NUCLEIC ACIDS ENCODING AND METHODS OF USE
- (iii) NUMBER OF SEQUENCES: 75
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Seed Intellectual Property Law Group
  - (B) STREET: Suite 6300, 701 Fifth Avenue
  - (C) CITY: Seattle
  - (D) STATE: Washington
  - (E) COUNTRY: USA
  - (F) ZIP: 98104
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US
  - (B) FILING DATE: 22-SEPT-2003
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Laherty, Carol D.
  - (B) REGISTRATION NUMBER: 51,909
  - (C) REFERENCE/DOCKET NUMBER: 480140.424D1
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (206) 622-4900
  - (B) TELEFAX: (206) 682-6031

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1700 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ix) FEATURE:
  - (A) NAME/KEY: CDS

(B) LOCATION: 148..1584

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..1700
- (D) OTHER INFORMATION: /note= "Mch4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGAAGTCTCT TCCCAAGCAA ATGGGAGCTT CTTTGACCT TGGAGCACAC AGAGGATTCT	60
ACTTTCTTTA AAACTTTGTT TTCAGGCAAT TTCCCTGAGA ACCGTTTACT TCCAGAAGAT	120
TGGTGGAGCT TGATCTGAAG GCTGGCC ATG AAA TCT CAA GGT CAA CAT TGG	171
Met Lys Ser Gln Gly Gln His Trp	
1 5	
TAT TCC AGT TCA GAT AAA AAC TGT AAA GTG AGC TTT CGT GAG AAG CTT	219
Tyr Ser Ser Ser Asp Lys Asn Cys Lys Val Ser Phe Arg Glu Lys Leu	
10 15 20	
CTG ATT ATT GAT TCA AAC CTG GGG GTC CAA GAT GTG GAG AAC CTC AAG	267
Leu Ile Ile Asp Ser Asn Leu Gly Val Gln Asp Val Glu Asn Leu Lys	
25 30 35 40	
TTT CTC TGC ATA GGA TTG GTC CCC AAC AAG AAG CTG GAG AAG TCC AGC	315
Phe Leu Cys Ile Gly Leu Val Pro Asn Lys Lys Leu Glu Lys Ser Ser	
45 50 55	
TCA GCC TCA GAT GTT TTT GAA CAT CTC TTG GCA GAG GAT CTG CTG AGT	363
Ser Ala Ser Asp Val Phe Glu His Leu Leu Ala Glu Asp Leu Leu Ser	
60 65 70	
GAG GAA GAC CCT TTC TTC CTG GCA GAA CTC CTC TAT ATC ATA CGG CAG	411
Glu Glu Asp Pro Phe Phe Leu Ala Glu Leu Leu Tyr Ile Ile Arg Gln	
75 80 85	
AAG AAG CTG CTG CAG CAC CTC AAC TGT ACC AAA GAG GAA GTG GAG CGA	459
Lys Lys Leu Leu Gln His Leu Asn Cys Thr Lys Glu Glu Val Glu Arg	
90 95 100	
CTG CTG CCC ACC CGA CAA AGG GTT TCT CTG TTT AGA AAC CTG CTC TAC	507
Leu Leu Pro Thr Arg Gln Arg Val Ser Leu Phe Arg Asn Leu Leu Tyr	
105 110 115 120	
GAA CTG TCA GAA GGC ATT GAC TCA GAG AAC TTA AAG GAC ATG ATC TTC	555
Glu Leu Ser Glu Gly Ile Asp Ser Glu Asn Leu Lys Asp Met Ile Phe	
125 130 135	
CTT CTG AAA GAC TCG CTT CCC AAA ACT GAA ATG ACC TCC CTA AGT TTC	603
Leu Leu Lys Asp Ser Leu Pro Lys Thr Glu Met Thr Ser Leu Ser Phe	
140 145 150	
CTG GCA TTT CTA GAG AAA CAA GGT AAA ATA GAT GAA GAT AAT CTG ACA	651
Leu Ala Phe Leu Glu Lys Gln Gly Lys Ile Asp Glu Asp Asn Leu Thr	
155 160 165	

TGC CTG GAG GAC CTC TGC AAA ACA GTT GTA CCT AAA CTT TTG AGA AAC Cys Leu Glu Asp Leu Cys Lys Thr Val Val Pro Lys Leu Leu Arg Asn 170 175 180	699
ATA GAG AAA TAC AAA AGA GAG AAA GCT ATC CAG ATA GTG ACA CCT CCT Ile Glu Lys Tyr Lys Arg Glu Lys Ala Ile Gln Ile Val Thr Pro Pro 185 190 195 200	747
GTA GAC AAG GAA GCC GAG TCG TAT CAA GGA GAG GAA GAA CTA CTT TCC Val Asp Lys Glu Ala Glu Ser Tyr Gln Gly Glu Glu Glu Leu Val Ser 205 210 215	795
CAA ACA GAT GTT AAG ACA TTC TTG GAA GCC TTA CCG AGG GCA GCT GTG Gln Thr Asp Val Lys Thr Phe Leu Glu Ala Leu Pro Arg Ala Ala Val 220 225 230	843
TAC AGG ATG AAT CGG AAC CAC AGA GGC CTC TGT GTC ATT GTC AAC AAC Tyr Arg Met Asn Arg Asn His Arg Gly Leu Cys Val Ile Val Asn Asn 235 240 245	891
CAC AGC TTT ACC TCC CTG AAG GAC AGA CAA GGA ACC CAT AAA GAT GCT His Ser Phe Thr Ser Leu Lys Asp Arg Gln Gly Thr His Lys Asp Ala 250 255 260	939
GAG ATC CTG AGT CAT GTG TTC CAG TGG CTT GGG TTC ACA GTG CAT ATA Glu Ile Leu Ser His Val Phe Gln Trp Leu Gly Phe Thr Val His Ile 265 270 275 280	987
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CTG ACC CAT GGG AGA TTT GGA GCT GTC TAC TCT TCG GAT GAG GCC CTC Leu Thr His Gly Arg Phe Gly Ala Val Tyr Ser Ser Asp Glu Ala Leu 315 320 325	1131
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AGA CTG GCT GAA AAA CCT AAA CTC TTT TTC ATC CAG GCC TGC CAA GGT Arg Leu Ala Glu Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gln Gly 345 350 355 360	1227
GAA GAG ATA CAG CCT TCC GTA TCC ATC GAA GCA GAT GCT CTG AAC CCT Glu Glu Ile Gln Pro Ser Val Ser Ile Glu Ala Asp Ala Leu Asn Pro 365 370 375	1275
GAG CAG GCA CCC ACT TCC CTG CAG GAC AGT ATT CCT GCC GAG GCT GAC Glu Gln Ala Pro Thr Ser Leu Gln Asp Ser Ile Pro Ala Glu Ala Asp 380 385 390	1323

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Phe Leu Leu Gly Leu Ala Thr Val Pro Gly Tyr Val Ser Phe Arg His	
395 400 405	
GTG GAG GAA GGC AGC TGG TAT ATT CAG TCT CTG TGT AAT CAT CTG AAG	1419
Val Glu Glu Gly Ser Trp Tyr Ile Gln Ser Leu Cys Asn His Leu Lys	
410 415 420	
AAA TTG GTC CCA AGA CAT GAA GAC ATC TTA TCC ATC CTC ACT GCT GTC	1467
Lys Leu Val Pro Arg His Glu Asp Ile Leu Ser Ile Leu Thr Ala Val	
425 430 435 440	
AAC GAT GAT GTG AGT CGA AGA GTG GAC AAA CAG GGA ACA AAG AAA CAG	1515
Asn Asp Asp Val Ser Arg Arg Val Asp Lys Gln Gly Thr Lys Lys Gln	
445 450 455	
ATG CCC CAG CCT GCT TTC ACA CTA AGG AAA AAA CTA GTA TTC CCT GTG	1563
Met Pro Gln Pro Ala Phe Thr Leu Arg Lys Lys Leu Val Phe Pro Val	
460 465 470	
CCC CTG GAT GCA CTT TCA ATA TAGCAGAGAG TTTTGTGNTGG TTCTTAGACC	1614
Pro Leu Asp Ala Leu Ser Ile	
475	
TCAAACGAAT CATTGGNTAT AACCTCCAGC CTCCTGCCCA GCACAGGAAT CGGTGGTCTC	1674
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## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Lys	Ser	Gln	Gly	Gln	His	Trp	Tyr	Ser	Ser	Ser	Asp	Lys	Asn	Cys
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Lys	Val	Ser	Phe	Arg	Glu	Lys	Leu	Leu	Ile	Ile	Asp	Ser	Asn	Leu	Glv
			20					25					30		
Val	Gln	Asp	Val	Glu	Asn	Leu	Lys	Phe	Leu	Cys	Ile	Gly	Leu	Val	Pro
		35					40					45			
Asn	Lys	Lys	Leu	Glu	Lys	Ser	Ser	Ser	Ala	Ser	Asp	Val	Phe	Glu	His
	50					55					60				
Leu	Leu	Ala	Glu	Asp	Leu	Leu	Ser	Glu	Glu	Asp	Pro	Phe	Phe	Leu	Ala
65					70					75					80
Glu	Leu	Leu	Tyr	Ile	Ile	Arg	Gln	Lys	Lys	Leu	Leu	Gln	His	Leu	Asn
				85					90					95	

Cys Thr Lys Glu Glu Val Glu Arg Leu Leu Pro Thr Arg Gln Arg Val  
 100 105 110  
 Ser Leu Phe Arg Asn Leu Leu Tyr Glu Leu Ser Glu Gly Ile Asp Ser  
 115 120 125  
 Glu Asn Leu Lys Asp Met Ile Phe Leu Leu Lys Asp Ser Leu Pro Lys  
 130 135 140  
 Thr Glu Met Thr Ser Leu Ser Phe Leu Ala Phe Leu Glu Lys Gln Gly  
 145 150 155 160  
 Lys Ile Asp Glu Asp Asn Leu Thr Cys Leu Glu Asp Leu Cys Lys Thr  
 165 170 175  
 Val Val Pro Lys Leu Leu Arg Asn Ile Glu Lys Tyr Lys Arg Glu Lys  
 180 185 190  
 Ala Ile Gln Ile Val Thr Pro Pro Val Asp Lys Glu Ala Glu Ser Tyr  
 195 200 205  
 Gln Gly Glu Glu Glu Leu Val Ser Gln Thr Asp Val Lys Thr Phe Leu  
 210 215 220  
 Glu Ala Leu Pro Arg Ala Ala Val Tyr Arg Met Asn Arg Asn His Arg  
 225 230 235 240  
 Gly Leu Cys Val Ile Val Asn Asn His Ser Phe Thr Ser Leu Lys Asp  
 245 250 255  
 Arg Gln Gly Thr His Lys Asp Ala Glu Ile Leu Ser His Val Phe Gln  
 260 265 270  
 Trp Leu Gly Phe Thr Val His Ile His Asn Asn Val Thr Lys Val Glu  
 275 280 285  
 Met Glu Met Val Leu Gln Lys Gln Lys Cys Asn Pro Ala His Ala Asp  
 290 295 300  
 Gly Asp Cys Phe Val Phe Cys Ile Leu Thr His Gly Arg Phe Gly Ala  
 305 310 315 320  
 Val Tyr Ser Ser Asp Glu Ala Leu Ile Pro Ile Arg Glu Ile Met Ser  
 325 330 335  
 His Phe Thr Ala Leu Gln Cys Pro Arg Leu Ala Glu Lys Pro Lys Leu  
 340 345 350  
 Phe Phe Ile Gln Ala Cys Gln Gly Glu Glu Ile Gln Pro Ser Val Ser  
 355 360 365  
 Ile Glu Ala Asp Ala Leu Asn Pro Glu Gln Ala Pro Thr Ser Leu Gln  
 370 375 380  
 Asp Ser Ile Pro Ala Glu Ala Asp Phe Leu Leu Gly Leu Ala Thr Val  
 385 390 395 400

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1883 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(A) NAME/KEY: CDS  
(B) LOCATION: 257..1744

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(A) NAME/KEY: misc feature
(B) LOCATION: 1.1883
(D) OTHER INFORMATION: /note= "Mch5"
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TGAAGGCTGG	TTGTTTCAGAC	TGAGCTTCCT	GCCTGCCTGT	ACCCCGCCAA	CAGCTTCAGA	60										
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TTGGCCGCCT	GAGCCCTTGA	GTTGGTCACT	TGAACCTTGG	GAATATTGAG	ATTATATTCT	240										
CCTGCCTTTT	AAAAAG	ATG	GAC	TTC	AGC	AGA	AAT	CTT	TAT	GAT	ATT	GGG	289			
		Met	Asp	Phe	Ser	Arg	Asn	Leu	Tyr	Asp	Ile	Gly				
		1				5						10				
GAA	CAA	CTG	GAC	AGT	GAA	GAT	CTG	GCC	TCC	CTC	AAG	TTC	CTG	AGC	CTG	337
Glu	Gln	Leu	Asp	Ser	Glu	Asp	Leu	Ala	Ser	Leu	Lys	Phe	Leu	Ser	Leu	
			15					20					25			
GAC	TAC	ATT	CCG	CAA	AGG	AAG	CAA	GAA	CCC	ATC	AAG	GAT	GCC	TTG	ATG	385
Asp	Tyr	Ile	Pro	Gln	Arg	Lys	Gln	Glu	Pro	Ile	Lys	Asp	Ala	Leu	Met	
			30				35					40				

TTA	TTC	CAG	AGA	CTC	CAG	GAA	AAG	AGA	ATG	TTG	GAG	GAA	AGC	AAT	CTG	433
Leu	Phe	Gln	Arg	Leu	Gln	Glu	Lys	Arg	Met	Leu	Glu	Glu	Ser	Asn	Leu	
	45					50					55					
TCC	TTC	CTG	AAG	GAG	CTG	CTC	TTC	CGA	ATT	AAT	AGA	CTG	GAT	TTG	CTG	481
Ser	Phe	Leu	Lys	Glu	Leu	Leu	Phe	Arg	Ile	Asn	Arg	Leu	Asp	Leu	Leu	
60					65				70						75	
ATT	ACC	TAC	CTA	AAC	ACT	AGA	AAG	GAG	GAG	ATG	GAA	AGG	GAA	CTT	CAG	529
Ile	Thr	Tyr	Leu	Asn	Thr	Arg	Lys	Glu	Glu	Met	Glu	Arg	Glu	Leu	Gln	
				80				85						90		
ACA	CCA	GGC	AGG	GCT	CAA	ATT	TCT	GCC	TAC	AGG	TTC	CAC	TTC	TGC	CGC	577
Thr	Pro	Gly	Arg	Ala	Gln	Ile	Ser	Ala	Tyr	Arg	Phe	His	Phe	Cys	Arg	
			95					100					105			
ATG	AGC	TGG	GCT	GAA	GCA	AAC	AGC	CAG	TGC	CAG	ACA	CAG	TCT	GTA	CCT	625
Met	Ser	Trp	Ala	Glu	Ala	Asn	Ser	Gln	Cys	Gln	Thr	Gln	Ser	Val	Pro	
		110					115					120				
TTC	TGG	CGG	AGG	GTC	GAT	CAT	CTA	TTA	ATA	AGG	GTC	ATG	CTC	TAT	CAG	673
Phe	Trp	Arg	Arg	Val	Asp	His	Leu	Leu	Ile	Arg	Val	Met	Leu	Tyr	Gln	
	125					130					135					
ATT	TCA	GAA	GAA	GTG	AGC	AGA	TCA	GAA	TTG	AGG	TCT	TTT	AAG	TTT	CTT	721
Ile	Ser	Glu	Glu	Val	Ser	Arg	Ser	Glu	Leu	Arg	Ser	Phe	Lys	Phe	Leu	
140					145					150					155	
TTG	CAA	GAG	GAA	ATC	TCC	AAA	TGC	AAA	CTG	GAT	GAT	GAC	ATG	AAC	CTG	769
Leu	Gln	Glu	Glu	Ile	Ser	Lys	Cys	Lys	Leu	Asp	Asp	Asp	Met	Asn	Leu	
				160					165					170		
CTG	GAT	ATT	TTC	ATA	GAG	ATG	GAG	AAG	AGG	GTC	ATC	CTG	GGA	GAA	GGA	817
Leu	Asp	Ile	Phe	Ile	Glu	Met	Glu	Lys	Arg	Val	Ile	Leu	Gly	Glu	Gly	
			175					180					185			
AAG	TTG	GAC	ATC	CTG	AAA	AGA	GTC	TGT	GCC	CAA	ATC	AAC	AAG	AGC	CTG	865
Lys	Leu	Asp	Ile	Leu	Lys	Arg	Val	Cys	Ala	Gln	Ile	Asn	Lys	Ser	Leu	
		190					195					200				
CTG	AAG	ATA	ATC	AAC	GAC	TAT	GAA	GAA	TTC	AGC	AAA	GGG	GAG	GAG	TTG	913
Leu	Lys	Ile	Ile	Asn	Asp	Tyr	Glu	Glu	Phe	Ser	Lys	Gly	Glu	Glu	Leu	
	205					210					215					
TGT	GGG	GTA	ATG	ACG	ATG	TCG	GAC	TGT	CCA	AGA	GAA	CAG	GAT	AGT	GAA	961
Cys	Gly	Val	Met	Thr	Met	Ser	Asp	Cys	Pro	Arg	Glu	Gln	Asp	Ser	Glu	
220					225					230					235	
TCA	CAG	ACT	TTG	GAC	AAA	GTT	TAC	CAA	ATG	AAA	AGC	AAG	CCT	CGG	GGA	1009
Ser	Gln	Thr	Leu	Asp	Lys	Val	Tyr	Gln	Met	Lys	Ser	Lys	Pro	Arg	Gly	
				240				245						250		
TAC	TGT	CTG	ATC	ATC	AAC	AAT	CAC	AAT	TTT	GCA	AAA	GCA	CGG	GAG	AAA	1057
Tyr	Cys	Leu	Ile	Ile	Asn	Asn	His	Asn	Phe	Ala	Lys	Ala	Arg	Glu	Lys	
			255					260					265			

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GCA GGG GCT TTG ACC ACG ACC TTT GAA GAG CTT CAT TTT GAG ATC AAG Ala Gly Ala Leu Thr Thr Thr Phe Glu Glu Leu His Phe Glu Ile Lys 285 290 295	1153
CCC CAC CAT GAC TGC ACA GTA GAG CAA ATC TAT GAG ATT TTG AAA ATC Pro His His Asp Cys Thr Val Glu Gln Ile Tyr Glu Ile Leu Lys Ile 300 305 310 315	1201
TAC CAA CTC ATG GAC CAC AGT AAC ATG GAC TGC TTC ATC TGC TGT ATC Tyr Gln Leu Met Asp His Ser Asn Met Asp Cys Phe Ile Cys Cys Ile 320 325 330	1249
CTC TCC CAT GGA GAC AAG GGC ATC ATC TAT GGC ACT GAT GGA CAG GAG Leu Ser His Gly Asp Lys Gly Ile Ile Tyr Gly Thr Asp Gly Gln Glu 335 340 345	1297
GCC CCC ATC TAT GAG CTG ACA TCT CAG TTC ACT GGT TTG AAG TGC CCT Ala Pro Ile Tyr Glu Leu Thr Ser Gln Phe Thr Gly Leu Lys Cys Pro 350 355 360	1345
TCC CTT GCT GGA AAA CCC AAA GTG TTT TTT ATT CAG GCT TGT CAG GGG Ser Leu Ala Gly Lys Pro Lys Val Phe Phe Ile Gln Ala Cys Gln Gly 365 370 375	1393
GAT AAC TAC CAG AAA GGT ATA CCT GTT GAG ACT GAT TCA GAG GAG CAA Asp Asn Tyr Gln Lys Gly Ile Pro Val Glu Thr Asp Ser Glu Glu Gln 380 385 390 395	1441
CCC TAT TTA GAA ATG GAT TTA TCA TCA CCT CAA ACG AGA TAT ATC CCG Pro Tyr Leu Glu Met Asp Leu Ser Ser Pro Gln Thr Arg Tyr Ile Pro 400 405 410	1489
GAT GAG GCT GAC TTT CTG CTG GGG ATG GCC ACT GTG AAT AAC TGT GTT Asp Glu Ala Asp Phe Leu Leu Gly Met Ala Thr Val Asn Asn Cys Val 415 420 425	1537
TCC TAC CGA AAC CCT GCA GAG GGA ACC TGG TAC ATC CAG TCA CTT TGC Ser Tyr Arg Asn Pro Ala Glu Gly Thr Trp Tyr Ile Gln Ser Leu Cys 430 435 440	1585
CAG AGC CTG AGA GAG CGA TGT CCT CGA GGC GAT GAT ATT CTC ACC ATC Gln Ser Leu Arg Glu Arg Cys Pro Arg Gly Asp Asp Ile Leu Thr Ile 445 450 455	1633
CTG ACT GAA GTG AAC TAT GAA GTA AGC AAC AAG GAT GAC AAG AAA AAC Leu Thr Glu Val Asn Tyr Glu Val Ser Asn Lys Asp Asp Lys Lys Asn 460 465 470 475	1681
ATG GGG AAA CAG ATG CCT CAG CCT ACT TTC ACA CTA AGA AAA AAA CTT Met Gly Lys Gln Met Pro Gln Pro Thr Phe Thr Leu Arg Lys Lys Leu 480 485 490	1729
GTC TTC CCT TCT GAT TGATGGTGCT ATTTTGTTTG TTTTGTTTTG TTTTGTTTTT	1784



Val Phe Pro Ser Asp  
495

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asp	Phe	Ser	Arg	Asn	Leu	Tyr	Asp	Ile	Gly	Glu	Gln	Leu	Asp	Ser	
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Glu	Asp	Leu	Ala	Ser	Leu	Lys	Phe	Leu	Ser	Leu	Asp	Tyr	Ile	Pro	Gln	
		20						25					30			
Arg	Lys	Gln	Glu	Pro	Ile	Lys	Asp	Ala	Leu	Met	Leu	Phe	Gln	Arg	Leu	
		35					40					45				
Gln	Glu	Lys	Arg	Met	Leu	Glu	Glu	Ser	Asn	Leu	Ser	Phe	Leu	Lys	Glu	
	50					55				60						
Leu	Leu	Phe	Arg	Ile	Asn	Arg	Leu	Asp	Leu	Leu	Ile	Thr	Tyr	Leu	Asn	
65					70					75					80	
Thr	Arg	Lys	Glu	Glu	Met	Glu	Arg	Glu	Leu	Gln	Thr	Pro	Gly	Arg	Ala	
			85						90					95		
Gln	Ile	Ser	Ala	Tyr	Arg	Phe	His	Phe	Cys	Arg	Met	Ser	Trp	Ala	Glu	
		100						105					110			
Ala	Asn	Ser	Gln	Cys	Gln	Thr	Gln	Ser	Val	Pro	Phe	Trp	Arg	Arg	Val	
		115					120					125				
Asp	His	Leu	Leu	Ile	Arg	Val	Met	Leu	Tyr	Gln	Ile	Ser	Glu	Glu	Val	
	130					135					140					
Ser	Arg	Ser	Glu	Leu	Arg	Ser	Phe	Lys	Phe	Leu	Leu	Gln	Glu	Glu	Ile	
145					150					155					160	
Ser	Lys	Cys	Lys	Leu	Asp	Asp	Asp	Met	Asn	Leu	Leu	Asp	Ile	Phe	Ile	
			165					170						175		
Glu	Met	Glu	Lys	Arg	Val	Ile	Leu	Gly	Glu	Gly	Lys	Leu	Asp	Ile	Leu	
		180						185					190			
Lys	Arg	Val	Cys	Ala	Gln	Ile	Asn	Lys	Ser	Leu	Leu	Lys	Ile	Ile	Asn	
		195					200					205				

Asp Tyr Glu Glu Phe Ser Lys Gly Glu Glu Leu Cys Gly Val Met Thr  
 210 215 220  
 Met Ser Asp Cys Pro Arg Glu Gln Asp Ser Glu Ser Gln Thr Leu Asp  
 225 230 235 240  
 Lys Val Tyr Gln Met Lys Ser Lys Pro Arg Gly Tyr Cys Leu Ile Ile  
 245 250 255  
 Asn Asn His Asn Phe Ala Lys Ala Arg Glu Lys Val Pro Lys Leu His  
 260 265 270  
 Ser Ile Arg Asp Arg Asn Gly Thr His Leu Asp Ala Gly Ala Leu Thr  
 275 280 285  
 Thr Thr Phe Glu Glu Leu His Phe Glu Ile Lys Pro His His Asp Cys  
 290 295 300  
 Thr Val Glu Gln Ile Tyr Glu Ile Leu Lys Ile Tyr Gln Leu Met Asp  
 305 310 315 320  
 His Ser Asn Met Asp Cys Phe Ile Cys Cys Ile Leu Ser His Gly Asp  
 325 330 335  
 Lys Gly Ile Ile Tyr Gly Thr Asp Gly Gln Glu Ala Pro Ile Tyr Glu  
 340 345 350  
 Leu Thr Ser Gln Phe Thr Gly Leu Lys Cys Pro Ser Leu Ala Gly Lys  
 355 360 365  
 Pro Lys Val Phe Phe Ile Gln Ala Cys Gln Gly Asp Asn Tyr Gln Lys  
 370 375 380  
 Gly Ile Pro Val Glu Thr Asp Ser Glu Glu Gln Pro Tyr Leu Glu Met  
 385 390 395 400  
 Asp Leu Ser Ser Pro Gln Thr Arg Tyr Ile Pro Asp Glu Ala Asp Phe  
 405 410 415  
 Leu Leu Gly Met Ala Thr Val Asn Asn Cys Val Ser Tyr Arg Asn Pro  
 420 425 430  
 Ala Glu Gly Thr Trp Tyr Ile Gln Ser Leu Cys Gln Ser Leu Arg Glu  
 435 440 445  
 Arg Cys Pro Arg Gly Asp Asp Ile Leu Thr Ile Leu Thr Glu Val Asn  
 450 455 460  
 Tyr Glu Val Ser Asn Lys Asp Asp Lys Lys Asn Met Gly Lys Gln Met  
 465 470 475 480  
 Pro Gln Pro Thr Phe Thr Leu Arg Lys Lys Leu Val Phe Pro Ser Asp  
 485 490 495

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..19
  - (D) OTHER INFORMATION: /note= "t96-pr1"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCAGCCTCGG CAGGAATAC

19

- (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..17
  - (D) OTHER INFORMATION: /note= "SK-Zap"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAGGAATTCG GCACGAG

17

- (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..18
  - (D) OTHER INFORMATION: /note= "Mch5-pr1"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GACAGAGCGA GATTCTGT

18

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "Mch5-pr2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCACCATCAA TCAGAAGG

18

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "Mch5-pr5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGAGATCA TGTCTCAC

18

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln Ala Cys Gln Gly

1

5

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gln Ala Cys Arg Gly  
 1                      5

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..6
  - (D) OTHER INFORMATION: /note= "Mch5"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Arg Asp Arg Asn Gly Thr  
 1                      5

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..6
  - (D) OTHER INFORMATION: /note= "Mch5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Leu Ser His Gly Asp Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..9  
(D) OTHER INFORMATION: /note= "Mch5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Phe Ile Gln Ala Cys Gln Gly Asp Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..5  
(D) OTHER INFORMATION: /note= "Mch5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val Glu Thr Asp Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "Mch5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asn	Cys	Val	Ser	Tyr	Arg	Asn	Pro	Ala	Glu	Gly	Thr	Trp	Tyr	Ile
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "Mch4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys	Asp	Arg	Gln	Gly	Thr
1				5	

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "Mch4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Thr His Gly Arg Phe

1

5

## (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..9
  - (D) OTHER INFORMATION: /note= "Mch4"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Phe Ile Gln Ala Cys Gln Gly Glu Glu  
 1                      5

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..5
  - (D) OTHER INFORMATION: /note= "Mch4"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ile Glu Ala Asp Ala  
 1                      5

## (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..15  
 (D) OTHER INFORMATION: /note= "Mch4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gly	Tyr	Val	Ser	Phe	Arg	His	Val	Glu	Glu	Gly	Ser	Trp	Tyr	Ile
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..6  
 (D) OTHER INFORMATION: /note= "Mch3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gly	Val	Arg	Asn	Gly	Thr
1				5	

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..6  
 (D) OTHER INFORMATION: /note= "Mch3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Leu	Ser	His	Gly	Glu	Glu
1				5	

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..9
  - (D) OTHER INFORMATION: /note= "Mch3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Phe	Ile	Gln	Ala	Cys	Arg	Gly	Thr	Glu
1				5				

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..5
  - (D) OTHER INFORMATION: /note= "Mch3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ile	Gln	Ala	Asp	Ser
1			5	

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..15
  - (D) OTHER INFORMATION: /note= "Mch3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gly	Tyr	Tyr	Ser	Trp	Arg	Ser	Pro	Gly	Arg	Gly	Ser	Trp	Phe	Val
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..6  
 (D) OTHER INFORMATION: /note= "Mch2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Pro	Glu	Arg	Arg	Gly	Thr
1				5	

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..6  
 (D) OTHER INFORMATION: /note= "Mch2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Leu	Ser	His	Gly	Glu	Gly
1				5	

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 9 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
- (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..6
  - (D) OTHER INFORMATION: /note= "Mch2"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
- ```

Ile Ile Gln Ala Cys Arg Gly Asn Gln
1           5

```
- (2) INFORMATION FOR SEQ ID NO:30:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
- (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..5
  - (D) OTHER INFORMATION: /note= "Mch2"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
- ```

Thr Glu Val Asp Ala
1           5

```
- (2) INFORMATION FOR SEQ ID NO:31:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
- (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..15
  - (D) OTHER INFORMATION: /note= "Mch2"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Gly Tyr Tyr Ser His Arg Glu Thr Val Asn Gly Ser Trp Tyr Ile  
 1                      5                      10                      15

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..6
  - (D) OTHER INFORMATION: /note= "CPP32"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Thr Ser Arg Ser Gly Thr  
 1                      5

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..6
  - (D) OTHER INFORMATION: /note= "CPP32"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Leu Ser His Gly Glu Glu  
 1                      5

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..9  
 (D) OTHER INFORMATION: /note= "CPP32"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ile Ile Gln Ala Cys Arg Gly Thr Glu  
 1 5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..5  
 (D) OTHER INFORMATION: /note= "CPP32"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ile Glu Thr Asp Ser  
 1 5

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..15  
 (D) OTHER INFORMATION: /note= "CPP32"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Tyr Tyr Ser Trp Arg Asn Ser Lys Asp Gly Ser Trp Phe Ile  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..6
  - (D) OTHER INFORMATION: /note= "CED-3"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:
 

Pro Thr Arg Asn Gly Thr  
 1                      5
- (2) INFORMATION FOR SEQ ID NO:38:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 6 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 1..6
    - (D) OTHER INFORMATION: /note= "CED-3"
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
 

Leu Ser His Gly Glu Glu  
 1                      5
- (2) INFORMATION FOR SEQ ID NO:39:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 9 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 1..9

(D) OTHER INFORMATION: /note= "CED-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Phe Val Gln Ala Cys Arg Gly Glu Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..5  
 (D) OTHER INFORMATION: /note= "CED-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Asp Ser Val Asp Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..15  
 (D) OTHER INFORMATION: /note= "CED-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Gln Tyr Val Ser Trp Arg Asn Ser Ala Arg Gly Ser Trp Phe Ile  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid



- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..6
  - (D) OTHER INFORMATION: /note= "ICE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```
Pro Arg Arg Thr Gly Ala
1           5
```

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..6
  - (D) OTHER INFORMATION: /note= "ICE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
Met Ser His Gly Ile Arg
1           5
```

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..9
  - (D) OTHER INFORMATION: /note= "ICE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ile Ile Gln Ala Cys Arg Gly Asp Ser  
 1 5

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..5  
 (D) OTHER INFORMATION: /note= "ICE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Trp Phe Lys Asp Ser  
 1 5

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..15  
 (D) OTHER INFORMATION: /note= "ICE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Asp Asn Val Ser Trp Arg His Pro Thr Met Gly Ser Val Phe Ile  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..6  
 (D) OTHER INFORMATION: /note= "TX"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Pro Pro Arg Asn Gly Ala  
 1 5

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..6  
 (D) OTHER INFORMATION: /note= "TX"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Ser His Gly Ile Leu  
 1 5

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 9 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..9  
 (D) OTHER INFORMATION: /note= "TX"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ile Val Gln Ala Cys Arg Gly Ala Asn  
 1 5

## (2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..5
  - (D) OTHER INFORMATION: /note= "TX"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Trp Val Lys Asp Ser  
1 5

## (2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..15
  - (D) OTHER INFORMATION: /note= "TX"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

His Asn Val Ser Trp Arg Asp Ser Thr Met Gly Ser Ile Phe Ile  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide

- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "ICErelIII"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Pro Ala Arg Asn Gly Ala  
1                      5

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..6
  - (D) OTHER INFORMATION: /note= "ICErelIII"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met Ser His Gly Ile Leu  
1                      5

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..9
  - (D) OTHER INFORMATION: /note= "ICErelIII"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Ile Val Gln Ala Cys Arg Gly Glu Lys  
1                      5

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
- (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..5
  - (D) OTHER INFORMATION: /note= "ICErelIII"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Trp	Val	Arg	Asp	Ser
1				5

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
- (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..15
  - (D) OTHER INFORMATION: /note= "ICErelIII"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

His	Asn	Val	Ser	Trp	Arg	Asp	Arg	Thr	Arg	Gly	Ser	Ile	Phe	Ile
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
- (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..6
  - (D) OTHER INFORMATION: /note= "ICH-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Glu Phe Arg Ser Gly Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..6  
(D) OTHER INFORMATION: /note= "ICH-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu Ser His Gly Val Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..9  
(D) OTHER INFORMATION: /note= "ICH-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Phe Ile Gln Ala Cys Arg Gly Asp Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "ICH-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp Gln Gln Asp Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "ICH-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gly Thr Ala Ala Met Arg Asn Thr Lys Arg Gly Ser Trp Tyr Ile  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CCTACAGGAT CCACTTCTGC CGCATGAGC

29

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:  
ACTCCTCCCC TTTGCTGAAT TCTTAATAGT CGT

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: .
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: /note= "Mch4 A"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```

Val Ser Phe Arg Glu Lys Leu Leu Ile Ile Asp Ser Asn Leu Gly Val
1          5          10          15
Gln Asp Val Glu Asn Leu Lys Phe Leu Cys Ile Gly Leu Val Pro Asn
20          25          30
Lys Lys Leu Glu Lys Ser Ser Ser Ala Ser Asp Val Phe Glu His Leu
35          40          45
Leu Ala Glu Asp Leu Leu Ser Glu Glu Asp Pro Phe Phe Leu Ala Glu
50          55          60
Leu Leu Tyr Ile Ile Arg Gln Lys Lys Leu Leu Gln His Leu Asn
65          70          75

```

## (2) INFORMATION FOR SEQ ID NO:66:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: /note= "Mch5 A"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Ser Arg Asn Leu Tyr Asp Ile Gly Glu Gln Leu Asp Ser Glu Asp Leu
1          5          10          15
Ala Ser Leu Lys Phe Leu Ser Leu Asp Thr Ile Pro Gln Arg Lys Gln
20          25          30
Glu Pro Ile Lys Asp Ala Leu Met Leu Phe Gln Arg Leu Gln Glu Lys
35          40          45
Arg Met Leu Glu Glu Ser Asn Leu Ser Phe Leu Lys Glu Leu Leu Phe
50          55          60
Arg Ile Asn Arg Leu Asp Leu Leu Ile Thr Tyr
65          70          75

```

## (2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 78 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

- (ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..78  
 (D) OTHER INFORMATION: /note= "Mch4 B"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

Val Ser Leu Phe Arg Asn Leu Leu Tyr Glu Leu Ser Glu Gly Ile Asp
1          5          10          15
Ser Glu Asn Leu Lys Asp Met Ile Phe Leu Leu Lys Asp Ser Leu Pro
          20          25          30
Lys Thr Glu Met Thr Ser Leu Ser Phe Leu Ala Phe Leu Glu Lys Gln
          35          40          45
Gly Lys Ile Asp Glu Asp Asn Leu Thr Cys Leu Glu Asp Leu Cys Lys
          50          55          60
Thr Val Val Pro Lys Leu Leu Arg Asn Ile Glu Lys Tyr Lys
65          70          75

```

- (2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 79 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

- (ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..79  
 (D) OTHER INFORMATION: /note= "Mch5 B"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

Val Asp His Leu Leu Ile Arg Val Met Leu Tyr Gln Ile Ser Glu Glu
1          5          10          15
Val Ser Arg Ser Glu Leu Arg Ser Phe Lys Phe Leu Leu Gln Glu Glu
          20          25          30
Ile Ser Lys Cys Lys Leu Asp Asp Asp Met Asn Leu Leu Asp Ile Phe

```

35						40					45				
Ile	Glu	Met	Glu	Lys	Arg	Val	Ile	Leu	Gly	Glu	Gly	Lys	Leu	Asp	Ile
	50					55					60				
Leu	Lys	Arg	Val	Cys	Ala	Gln	Ile	Asn	Lys	Ser	Leu	Leu	Lys	Ile	
65					70					75					

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Gly Ser Trp Phe Ile  
1 5

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Gly Ser Trp Tyr Ile  
1 5

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Asp Glu Val Asp

1

## (2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Tyr Val Ala Asp  
1

## (2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Ile Glu Thr Asp Ser  
1 5

## (2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ile Gln Ala Asp Ala  
1 5

## (2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ile Glu Ala Asp Ala  
1 5